morphology producing ectopic "hinge points" that resemble the endogenous ventral midline hinge point — critical in bending, shaping and eventually closing the neural tube. Thus, we bring new insight into the mechanism underlying midbrain FP specification and show how *FOXA2* regulates both gene expression and cell shape.

doi:10.1016/j.ydbio.2008.05.498

Program/Abstract # 422
A transition in *Sox2* gene regulation distinguishes the epiblastic and anterior neural plate states
Makiko Iwafuchi, Tatsuya Takemoto, Masanori Uchikawa, Yusuke Kamachi, Hisato Kondoh
Department of Developmental Biology, Osaka University, Suita, Osaka, Japan

The transcription factor gene *Sox2* is expressed in the epiblast and neural plate during the early embryonic stages in amniotes. Among the number of enhancers regulating *Sox2*, N-2 is most responsible for *Sox2* expression in the epiblast and anterior neural plate, as homozygous deletion of enhancer N-2 abrogates expression of *Sox2* in these tissue primordia.Here, the minimal essential sequence (core sequence) of enhancer N-2 was identified. Functional analysis of the regulatory elements was done using various mutated versions of the core sequences as performed by transfecting ES cells (as epiblast substitutes) and electroporating stage 4–5 chicken embryos (to assess neural plate activity). This analysis identified three POU factor binding sites (two overlapping) and an OTX binding site in the coresequence, as confirmed by EMSA. In ES cells with strong OCT3/4 expression, the N-2 core enhancer was primarily dependent on the activity of OCT3/4. In contrast, in the anterior neural plate, where OCT3/4 is down-regulated and OTX2 is strongly activated, the enhancer was dependent on OTX2 activity. In the *Otx2* knockout embryo, *Sox2* was expressed in the epiblastic stage but not in the anterior neural plate stage. Thus, the transition of *Sox2* regulation from OCT3/4-dependence to OTX2-dependence distinguishes the epiblastic and anterior neural plate states in early ectodermal lineages.

doi:10.1016/j.ydbio.2008.05.499

Program/Abstract # 423
Detailed analysis of *zic1*, *zic2*, *zic3*, and *zic4* expression in trunk and hindbrain sections of early chick embryos
Ariel McMahon, Sara Muscarelli, Christa Merzdorf
Department of Cell Biology and Neuroscience, Montana State University, Bozeman, MT, USA

The Zic family of transcription factors plays multiple roles in early development. *zic* genes are highly conserved, particularly in their zinc finger domains and in the regions immediately surrounding the zinc fingers. Using published sequences and the chicken genome as guides, we have generated in situ probes that are specific for the *zic1*, *zic2*, *zic3*, and *zic4* genes in chick. We have previously presented whole mount in situ comparisons for *zic1* and *zic2* with preliminary data on *zic3* and *zic4*. Now we have studied the expression of *zic3* and *zic4* in greater detail and present a detailed analysis of *zic1–4* expression in sections of stage 14/15 and stage 18/19 embryos. The *zic1–3* genes are expressed in overlapping patterns in the dorsal neural tube and in the dorsomedial portion of the somites, while *zic4* is expressed in the forebrain, but not in the hindbrain or trunk. *zic2* is the first *zic* gene expressed in the dorsal neural tube upon neural tube formation. *zic1* is the earliest *zic* gene expressed during somitogenesis. *zic3* is uniquely expressed in the presomitic mesoderm, although it is not expressed in newly formed somites. *zic2* is uniquely expressed throughout the neural tube of the tail tip and in the periotic mesoderm. Other differences will be discussed, comparisons with *zic* gene expression in other organisms will be made, and the expression patterns will be related to phenotypes resulting from aberrant *zic* gene expression.

doi:10.1016/j.ydbio.2008.05.500

Program/Abstract # 424
Analysis of chicken paraxial mesoderm progenitor transcriptome using microarray technique
Bertrand Bénazéraf [a], Sachin Mathur [a], Karin Zueckert-Gaudenz [a], Gaye Hattem [a], Jayasinghe Sachintha [a], Tassy Olivier [a,b], Haug Jeff, Pourquié Olivier [a,b]
[a] *Stowers Institute for Medical Research, 1000 East 50th Street, Kansas City, Missouri 64110, USA*
[b] *Howard Hughes Medical Institute, Kansas City, MO 64110, USA*

The vertebrate body is subdivided along the antero-posterior axis into repeated segments. This pattern is established by the segmentation of the presomitic mesoderm (PSM) during embryogenesis. Cells that give rise to the PSM derive from the primitive streak and later from the tail bud. Because the segmentation process continues during antero-posterior (AP) axis elongation, the population of PSM cells must be continuously renewed. Different studies suggest the existence of paraxial mesoderm "stem cells" located first in the most anterior part of the primitive streak and then in the tail bud. While these cells appear to be of major importance in PSM production and in the set-up of the segmentation program, their cellular and molecular properties are not well understood. To better understand these properties, we use a DNA microarray approach in the chick embryo to identify genes specifically expressed in these precursors. Several candidate genes identified during this screen show specific expression in the zone of the paraxial progenitor stem cells by in situ hybridization. The function of these candidate genes will be tested in future work to know if whether or not they participate in the specific properties of paraxial mesoderm progenitors.

doi:10.1016/j.ydbio.2008.05.501

Program/Abstract # 425
Identifying novel targets of Ptf1a using ChIP-on-chip technology
Sherri-Gae Scott, Steven D. Leach
[a] *Department of Surgery, Johns Hopkins University School of Medicine, Baltimore, MD, USA*
[b] *Department of Cell Biology, Johns Hopkins University School of Medicine, Baltimore, MD, USA*

Ptf1a is a bHLH transcription factor that is expressed in the progenitor cells of the dorsal bud at the onset of pancreas development. These progenitor cells eventually give rise to pancreatic ducts, endocrine and exocrine cells. As the pancreas develops, Ptf1a also functions to induce and maintain differentiation of the exocrine pancreas. In order to gain additional insight into the role of Ptf1a in mouse pancreas development, we intend to identify novel targets of this transcription factor and to investigate their role in pancreas development. We used chromatin immunoprecipitation (ChIP) *in vivo* to investigate the interaction between Ptf1a and genomic DNA in adult mouse pancreas, liver was utilized as a control tissue not expressing